REMARKS

Status of the Claims

Claims 1-97 were pending. Claims 1-37, 40-44 and 46-97 were withdrawn pursuant to a Restriction Requirement that has been made FINAL and is discussed below. Claims 2, 3, 4 and 38 have been amended as shown above to make explicit that the polynucleotide of the expression cassettes exhibits at least 90% identity to the full-length of the sequence identified in the claim. Claims 78 and 91 have been amended to depend from examined claim 38. Claims 1, 5-37, 39-77 and 97 have been canceled without prejudice or disclaimer. Thus, claims 2-4, 38 and 78-96 are pending of which claim 38 has been examined.

Restriction Requirement

As noted above, the Restriction Requirement has been made FINAL. In this regard, the Examiner asserts that § 803.04 of the MPEP indicating that 10 sequences should be examined together is "only a guideline and not legally binding" and that this application is not eligible for this option because it is not a SPDI application. (Office Action, page 1).

As correctly noted by the Office, it is well settled that two criteria must be met for a proper restriction requirement under M.P.E.P. § 803: (1) the inventions must be independent or distinct as claimed; and (2) there must be a serious burden on the Examiner if restriction is not required. However, Applicants respectfully submit that the Examiner has not met this burden.

Here, given the high homology between the sequences, the Examiner cannot show that it would impart a serious burden to examine the sequences together. Indeed, the Examiner has not even shown that the nucleotide sequence encode "structurally different envelope glycoproteins" as asserted on page 2 of the Office Action. In fact, the sequences exhibit high homology to each other and a search of the art for sequences relevant to any of SEQ ID NOs:46, 47, 49, 97, 119, 120, 121, 122, 123, 124, 125, 126, 127, 131, 132, or 133 would necessarily reveal art relevant to the other sequences.

In this regard, Applicants again direct attention to the alignment of SEQ ID NOs:120 and 121 submitted with the Response to Restriction Requirement and submitted herewith again for the Examiner's convenience. In addition, Applicants attach hereto an alignment of all of the sequences recited in claim 38 along with SEQ ID NOs: 46 and 47 (claims 2 and 3, depicting common regions of Env). All of these sequences exhibit high homology to each other.

In view of the high degree of homology between the sequences of all the pending claims, it is clear that searching the art for the full-length of any of these sequences would necessarily reveal references relevant to all other sequences and, as such, it would not impart a serious burden on the Examiner to search them together. By contrast, it would certainly impart a serious financial burden

on Applicants to file individual applications to each highly-related sequence. No serious burden on the Examiner coupled with a very serious burden on Applicants does not meet the goal of Restriction practice.

Accordingly, Applicants again submit that the Restriction Requirement as between pending claims 2, 3, 4 and the individual sequences of claim 38 cannot stand because the two criteria of M.P.E.P. § 803 have not been fulfilled.

Thus, Applicants reiterate that claims 2-4 should be examined with claim 38. Furthermore, Applicants request rejoinder of process claims 78-96 when the elected product claims are found allowable.

Finally, Applicants expressly reserve their right under 35 USC §121 to file one or more divisional applications directed to the nonelected subject matter during the pendency of this application.

Sequence Listing

As the objection to the Sequence Listing was not reiterated, Applicants conclude that the Sequence Listing and accompanying computer readable form accompanying the Preliminary Amendment as filed on May 29, 2003 is acceptable.

IDS

The Examiner has requested, seemingly pursuant to 37 C.F.R. § 1.98(a)(3)(i), a statement identifying the relevance of each document cited in the IDS to the claimed invention. However, it is clear from this statute that such an explanation is required only for information listed that is <u>not in English</u> (37 C.F.R. 1.98(a)(3)(i)):

> A concise explanation of the relevance ...of each patent, publication or other information listed **that is not in the English language**. The concise explanation may be either separate from applicant's specification or incorporated therein.

Therefore, Applicants are <u>not</u> required to provide a concise application for any of the references cited in the IDS. Certainly, the Examiner must consider the IDS filed June 28, 2005, which contains only 8 references.

In sum, the documents submitted in the Information Disclosure Statements in this application should all be considered on their merits.

Inventorship

After the mailing of this Office Action (*i.e.*, on June 28, 2005), Applicants filed a Petition to Correct Inventorship and accompanying documents. Applicants request acknowledgment that the change in inventorship has been entered.

35 U.S.C. § 112, 1st Paragraph, Written Description

Previous claims 38, 39, and 45 were rejected under 35 U.S.C § 112, first paragraph as allegedly not described by the specification as filed. (Office Action, pages 2-5). In particular, it was asserted that the written description requirement was not satisfied because the claims did not limit the polynucleotide sequence to any particular length. *Id.*

By amendment herein, Applicants have amended the claims as shown above to specify that the sequences of the claimed expression cassettes much exhibit at least 90% identity to the full-length of the recited sequences (identified by SEQ ID NO). Thus, the rejection has been obviated.

CONCLUSION

In view of the foregoing amendments and remarks, Applicants submit that the claims are now in condition for allowance and request early notification to that effect.

Please direct all further written communications regarding this application to:

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P. O. Box 8097
Emeryville, CA 94662-8097
Telephone: (510) 923-2192
Facsimile: (510) 655-3542.

Respectfully submitted,

Date: August 30, 2005

By: _____

Dahna S. Pasternak
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SEQUENCE ANALYSIS

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ClustalW Results

Results of search	
Number of sequences	14
Alignment score	1075087
Sequence format	Pearson
Sequence type	nt
ClustalW version	1.82
JalView	
Output file	clustalw-20050726-22511744.output
Alignment file	clustalw-20050726-22511744.aln
Guide tree file	clustalw-20050726-22511744.dnd
Your input file	clustalw-20050726-22511744.input
SUBMIT ANOTHER JOB	

To save a result file right-click the file link in the above table and choose "Sa
If you cannot see the JalView button, reload the page and check your browse

Scores Table

Sort by | Sequence Number | View Output File

SeqA	Name	Len(nt)	SeqB	Name	Len(nt)	Score
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1	seqid46	97	5	seqid121	1986	97
1	seqid46	97	6	seqid122	2397	97
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1	seqid46	97	8	seqid124	2529	97

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1	seqid46	97	10	seqid126	2616	97
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1	seqid46	97	14	seqid133	2073	97
2	seqid47	144	3	seqid119	1473	96
2	seqid47	144	4	seqid120	1986	96
2	seqid47	144	5	seqid121	1986	96
2	seqid47	144	6	seqid122	2397	96
2	seqid47	144	7	seqid123	2529	96
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2	seqid47	144	11	seqid127	2616	96
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2	seqid47	144	14	seqid133	2073	96
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PLEASE NOTE: Some scores may be missing from the above table if the alig output.

Sort by | Sequence Number | View Output File

Alignment

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CLUSTAL W (1.82) multiple sequence alignment


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seqid46         ----------------------------------------------
seqid47         ----------------------------------------------
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seqid47         ------------------------------------------------
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seqid47         ----------------------------------------------
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seqid47         ----------------------------------------------
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seqid121        ----------
seqid132        ----------
seqid133        ----------
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seqid121        ----------
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seqid131        ----------

seqid119        ----------
seqid120        ----------
seqid121        ----------
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seqid131        ----------------------------------------------

seqid119        ----------------------------------------------
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seqid123        CATCCTGATCGCCGTGCGCGCCGTGGAGCTGCTGGGCCACAGCAGC
seqid124        CATCCTGATCGCCGTGCGCGCCGTGGAGCTGCTGGGCCACAGCAGC
seqid126        CATCCTGATCGCCGTGCGCGCCGTGGAGCTGCTGGGCCACAGCAGC
seqid127        CATCCTGATCGCCGTGCGCGCCGTGGAGCTGCTGGGCCACAGCAGC
seqid46         ----------------------------------------------
seqid47         ----------------------------------------------
seqid125        CATCCTGATCGCCGTGCGCGCCGTGGAGCTGCTGGGCCACAGCAGC
seqid131        ----------------------------------------------

seqid119        ----------------------------------------------
seqid120        ----------------------------------------------
seqid121        ----------------------------------------------
seqid132        ----------------------------------------------
seqid133        ----------------------------------------------
seqid122        GCGCGGCTGGGAGATCCTGAAGTACCTGGGCAGCCTGGTGCAGTAC
seqid123        GCGCGGCTGGGAGATCCTGAAGTACCTGGGCAGCCTGGTGCAGTAC
seqid124        GCGCGGCTGGGAGATCCTGAAGTACCTGGGCAGCCTGGTGCAGTAC
seqid126        GCGCGGCTGGGAGATCCTGAAGTACCTGGGCAGCCTGGTGCAGTAC
seqid127        GCGCGGCTGGGAGATCCTGAAGTACCTGGGCAGCCTGGTGCAGTAC
seqid46         ----------------------------------------------
seqid47         ----------------------------------------------
seqid125        GCGCGGCTGGGAGATCCTGAAGTACCTGGGCAGCCTGGTGCAGTAC
seqid131        ----------------------------------------------

seqid119        ----------------------------------------------
seqid120        ----------------------------------------------
seqid121        ----------------------------------------------
seqid132        ----------------------------------------------
seqid133        ----------------------------------------------
seqid122        GAAGAAGAGCGCCATCAGCCTGCTGGACACCATCGCCATCACCGTC
seqid123        GAAGAAGAGCGCCATCAGCCTGCTGGACACCATCGCCATCACCGTC
seqid124        GAAGAAGAGCGCCATCAGCCTGCTGGACACCATCGCCATCACCGTC
seqid126        GAAGAAGAGCGCCATCAGCCTGCTGGACACCATCGCCATCACCGTC
seqid127        GAAGAAGAGCGCCATCAGCCTGCTGGACACCATCGCCATCACCGTC
seqid46         ----------------------------------------------
seqid47         ----------------------------------------------
seqid125        GAAGAAGAGCGCCATCAGCCTGCTGGACACCATCGCCATCACCGTC
seqid131        ----------------------------------------------

seqid119        ----------------------------------------------
seqid120        ----------------------------------------------
seqid121        ----------------------------------------------
seqid132        ----------------------------------------------
```

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seqid133        ------------------------------------------------
seqid122        CCGCATCATCGAGCTGGTGCAGCGCATCTGCCGCGCCATCCTGAAC
seqid123        CCGCATCATCGAGCTGGTGCAGCGCATCTGCCGCGCCATCCTGAAC
seqid124        CCGCATCATCGAGCTGGTGCAGCGCATCTGCCGCGCCATCCTGAAC
seqid126        CCGCATCATCGAGCTGGTGCAGCGCATCTGCCGCGCCATCCTGAAC
seqid127        CCGCATCATCGAGCTGGTGCAGCGCATCTGCCGCGCCATCCTGAAC
seqid46         ------------------------------------------------
seqid47         ------------------------------------------------
seqid125        CCGCATCATCGAGCTGGTGCAGCGCATCTGCCGCGCCATCCTGAAC
seqid131        ------------------------------------------------


seqid119        ------------------------------------
seqid120        ------------------------------------
seqid121        ------------------------------------
seqid132        ------------------------------------
seqid133        ------------------------------------
seqid122        CCGCCAGGGCTTCGAGGCCGCCCTGCTGTAACTCGAG 2397
seqid123        CCGCCAGGGCTTCGAGGCCGCCCTGCTGTAACTCGAG 2529
seqid124        CCGCCAGGGCTTCGAGGCCGCCCTGCTGTAACTCGAG 2529
seqid126        CCGCCAGGGCTTCGAGGCCGCCCTGCTGTAACTCGAG 2616
seqid127        CCGCCAGGGCTTCGAGGCCGCCCTGCTGTAACTCGAG 2616
seqid46         ------------------------------------
seqid47         ------------------------------------
seqid125        CCGCCAGGGCTTCGAGGCCGCCCTGCTGTAACTCGAG 2613
seqid131        ------------------------------------
```

PLEASE NOTE: Showing colors on large alignments is slow.

Show Colors | View Alignment File

Guide Tree

Show as Phylogram Tree | Show Distances | View DND F

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(
(
(
(
(
(
seqid46:-0.00705,
seqid47:0.00705)
:0.00360,
(
seqid125:-0.00719,
seqid131:0.00817)
:0.02358)
:0.01417,
(
(
(
(
```

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seqid122:0.01713,
seqid123:-0.01713)
:0.00978,
seqid124:-0.00734)
:0.01374,
seqid126:-0.01249)
:0.00803,
seqid127:-0.00255)
:0.00380)
:0.00475,
seqid133:0.00545)
:0.00253,
seqid132:0.00078)
:0.00102,
(
seqid119:0.00677,
seqid120:-0.00066)
:0.00081,
seqid121:0.00274);
```
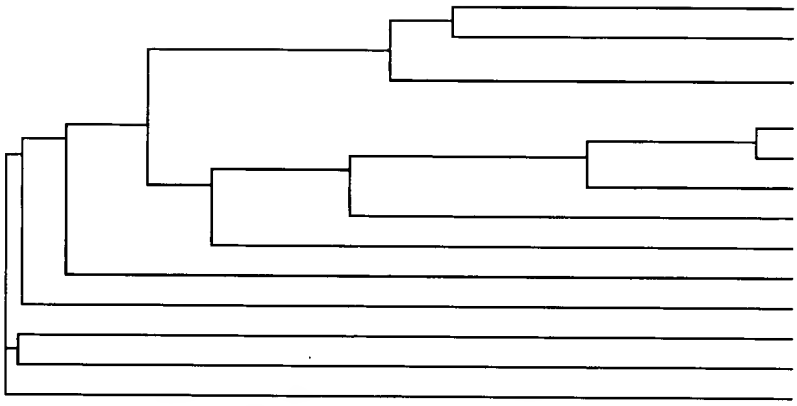

Cladogram



Right-click on the above tree to see display options.
Problems printing? Read how to print a Phylogram or Cladogram.

CLUSTAL W (1.82) multiple sequence alignment

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seqidno120      GAATTCATGCGCGTGATGGGCACCCAGAAGAACTGCCAGCAGTGGTGGATCTGGGGCATC 60
seqidno121      GAATTCATGCGCGTGATGGGCACCCAGAAGAACTGCCAGCAGTGGTGGATCTGGGGCATC 60
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seqidno120      CTGGGCTTCTGGATGCTGATGATCTGCAACACCGAGGACCTGTGGGTGACCGTGTACTAC 120
seqidno121      CTGGGCTTCTGGATGCTGATGATCTGCAACACCGAGGACCTGTGGGTGACCGTGTACTAC 120
                ************************************************************

seqidno120      GGCGTGCCCGTGTGGCGCGACGCCAAGACCACCCTGTTCTGCGCCAGCGACGCCAAGGCC 180
seqidno121      GGCGTGCCCGTGTGGCGCGACGCCAAGACCACCCTGTTCTGCGCCAGCGACGCCAAGGCC 180
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seqidno120      TACGAGACCGAGGTGCACAACGTGTGGGCCACCCACGCCTGCGTGCCCACCGACCCCAAC 240
seqidno121      TACGAGACCGAGGTGCACAACGTGTGGGCCACCCACGCCTGCGTGCCCACCGACCCCAAC 240
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seqidno120      CCCCAGGAGATCGTGCTGGGCAACGTGACCGAGAACTTCAACATGTGGAAGAACGACATG 300
seqidno121      CCCCAGGAGATCGTGCTGGGCAACGTGACCGAGAACTTCAACATGTGGAAGAACGACATG 300
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seqidno120      GCCGACCAGATGCACGAGGACGTGATCAGCCTGTGGGACCAGAGCCTGAAGCCCTGCGTG 360
seqidno121      GCCGACCAGATGCACGAGGACGTGATCAGCCTGTGGGACCAGAGCCTGAAGCCCTGCGTG 360
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seqidno120      AAGCTGACCCCCCTGTGCGTGACCCTGAACTGCACCGACACCAACGTGACCGGCAACCGC 420
seqidno121      AAGCTGACCCCCCTGTGCGTGACCCTGAACTGCACCGACACCAACGTGACCGGCAACCGC 420
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seqidno120      ACCGTGACCGGCAACAGCACCAACAACACCAACGGCACCGGCATCTACAACATCGAGGAG 480
seqidno121      ACCGTGACCGGCAACAGCACCAACAACACCAACGGCACCGGCATCTACAACATCGAGGAG 480
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seqidno120      ATGAAGAACTGCAGCTTCAACGCCGGCGCCGGCCGCCTGATCAACTGCAACACCAGCACC 540
seqidno121      ATGAAGAACTGCAGCTTCAACGCCGGCGCCGGCCGCCTGATCAACTGCAACACCAGCACC 540
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seqidno120      ATCACCCAGGCCTGCCCCAAGGTGAGCTTCGACCCCATCCCCATCCACTACTGCGCCCCC 600
seqidno121      ATCACCCAGGCCTGCCCCAAGGTGAGCTTCGACCCCATCCCCATCCACTACTGCGCCCCC 600
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seqidno120      GCCGGCTACGCCATCCTGAAGTGCAACAACAAGACCTTCAACGGCACCGGCCCCTGCTAC 660
seqidno121      GCCGGCTACGCCATCCTGAAGTGCAACAACAAGACCTTCAACGGCACCGGCCCCTGCTAC 660
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seqidno120      AACGTGAGCACCGTGCAGTGCACCCACGGCATCAAGCCCGTGGTGAGCACCCAGCTGCTG 720
seqidno121      AACGTGAGCACCGTGCAGTGCACCCACGGCATCAAGCCCGTGGTGAGCACCCAGCTGCTG 720
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seqidno120      CTGAACGGCAGCCTGGCCGAGGAGGGCATCATCATCCGCAGCGAGAACCTGACCGAGAAC 780
seqidno121      CTGAACGGCAGCCTGGCCGAGGAGGGCATCATCATCCGCAGCGAGAACCTGACCGAGAAC 780
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seqidno120      ACCAAGACCATCATCGTGCACCTGAACGAGAGCGTGGAGATCAACTGCACCCGCCCCAAC 840
seqidno121      ACCAAGACCATCATCGTGCACCTGAACGAGAGCGTGGAGATCAACTGCACCCGCCCCAAC 840
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seqidno120      AACAACACCCGCAAGAGCGTGCGCATCGGCCCCGGCCAGGCCTTCTACGCCACCAACGAC 900
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seqidno121      AACAACACCCGCAAGAGCGTGCGCATCGGCCCCGGCCAGGCCTTCTACGCCACCAACGAC 900
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seqidno120      GTGATCGGCAACATCCGCCAGGCCCACTGCAACATCAGCACCGACCGCTGGAACAAGACC 960
seqidno121      GTGATCGGCAACATCCGCCAGGCCCACTGCAACATCAGCACCGACCGCTGGAACAAGACC 960
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seqidno120      CTGCAGCAGGTGATGAAGAAGCTGGGCGAGCACTTCCCCAACAAGACCATCCAGTTCAAG 1020
seqidno121      CTGCAGCAGGTGATGAAGAAGCTGGGCGAGCACTTCCCCAACAAGACCATCCAGTTCAAG 1020
                ************************************************************

seqidno120      CCCCACGCCGGCGGCGACCTGGAGATCACCATGCACAGCTTCAACTGCCGCGGCGAGTTC 1080
seqidno121      CCCCACGCCGGCGGCGACCTGGAGATCACCATGCACAGCTTCAACTGCCGCGGCGAGTTC 1080
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seqidno120      TTCTACTGCAACACCAGCAACCTGTTCAACAGCACCTACCACAGCAACAACGGCACCTAC 1140
seqidno121      TTCTACTGCAACACCAGCAACCTGTTCAACAGCACCTACCACAGCAACAACGGCACCTAC 1140
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seqidno120      AAGTACAACGGCAACAGCAGCAGCCCCATCACCCTGCAGTGCAAGATCAAGCAGATCGTG 1200
seqidno121      AAGTACAACGGCAACAGCAGCAGCCCCATCACCCTGCAGTGCAAGATCAAGCAGATCGTG 1200
                ************************************************************

seqidno120      CGCATGTGGCAGGGCGTGGGCCAGGCCACCTACGCCCCCCCCATCGCCGGCAACATCACC 1260
seqidno121      CGCATGTGGCAGGGCGTGGGCCAGGCCACCTACGCCCCCCCCATCGCCGGCAACATCACC 1260
                ************************************************************

seqidno120      TGCCGCAGCAACATCACCGGCATCCTGCTGACCCGCGACGGCGGCTTCAACACCACCAAC 1320
seqidno121      TGCCGCAGCAACATCACCGGCATCCTGCTGACCCGCGACGGCGGCTTCAACACCACCAAC 1320
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seqidno120      AACACCGAGACCTTCCGCCCCGGCGGCGGCGACATGCGCGACAACTGGCGCAGCGAGCTG 1380
seqidno121      AACACCGAGACCTTCCGCCCCGGCGGCGGCGACATGCGCGACAACTGGCGCAGCGAGCTG 1380
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seqidno120      TACAAGTACAAGGTGGTGGAGATCAAGCCCCTGGGCATCGCCCCCACCAAGGCCAAGCGC 1440
seqidno121      TACAAGTACAAGGTGGTGGAGATCAAGCCCCTGGGCATCGCCCCCACCAAGGCCATCAGC 1440
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seqidno120      CGCGTGGTGCAGCGCGAGAAGCGCGCCGTGGGCATCGGCGCCGTGTTCCTGGGCTTCCTG 1500
seqidno121      AGCGTGGTGCAGAGCGAGAAGAGCGCCGTGGGCATCGGCGCCGTGTTCCTGGGCTTCCTG 1500
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seqidno120      GGCGCCGCCGGCAGCACCATGGGCGCCGCCAGCATCACCCTGACCGTGCAGGCCCGCCAG 1560
seqidno121      GGCGCCGCCGGCAGCACCATGGGCGCCGCCAGCATCACCCTGACCGTGCAGGCCCGCCAG 1560
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seqidno120      CTGCTGAGCGGCATCGTGCAGCAGCAGAGCAACCTGCTGAAGGCCATCGAGGCCCAGCAG 1620
seqidno121      CTGCTGAGCGGCATCGTGCAGCAGCAGAGCAACCTGCTGAAGGCCATCGAGGCCCAGCAG 1620
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seqidno120      CACATGCTGCAGCTGACCGTGTGGGGCATCAAGCAGCTGCAGGCCCGCGTGCTGGCCATC 1680
seqidno121      CACATGCTGCAGCTGACCGTGTGGGGCATCAAGCAGCTGCAGGCCCGCGTGCTGGCCATC 1680
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seqidno120      GAGCGCTACCTGAAGGACCAGCAGCTGCTGGGCATCTGGGGCTGCAGCGGCCGCCTGATC 1740
seqidno121      GAGCGCTACCTGAAGGACCAGCAGCTGCTGGGCATCTGGGGCTGCAGCGGCCGCCTGATC 1740
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seqidno120      TGCACCACCGCCGTGCCCTGGAACAGCAGCTGGAGCAACAAGAGCGAGAAGGACATCTGG 1800
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seqidno121      TGCACCACCGCCGTGCCCTGGAACAGCAGCTGGAGCAACAAGAGCGAGAAGGACATCTGG 1800
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seqidno120      GACAACATGACCTGGATGCAGTGGGACCGCGAGATCAGCAACTACACCGGCCTGATCTAC 1860
seqidno121      GACAACATGACCTGGATGCAGTGGGACCGCGAGATCAGCAACTACACCGGCCTGATCTAC 1860
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seqidno120      AACCTGCTGGAGGACAGCCAGAACCAGCAGGAGAAGAACGAGAAGGACCTGCTGGAGCTG 1920
seqidno121      AACCTGCTGGAGGACAGCCAGAACCAGCAGGAGAAGAACGAGAAGGACCTGCTGGAGCTG 1920
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seqidno120      GACAAGTGGAACAACCTGTGGAACTGGTTCGACATCAGCAACTGGCCCTGGTACATCTAA 1980
seqidno121      GACAAGTGGAACAACCTGTGGAACTGGTTCGACATCAGCAACTGGCCCTGGTACATCTAA 1980
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seqidno120      CTCGAG 1986
seqidno121      CTCGAG 1986
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